

(1) GENERAL INFORMATION:

- (i) APPLICANTS: Zimmermann, Rainer; Park, John E.;
Rettig, Wolfgang; Old, Lloyd J.
- (ii) TITLE OF INVENTION: ISOLATED DIMERIC FIBROBLAST ACTIVATION PROTEIN
ALPHA, AND USES THEREOF
- (iii) NUMBER OF SEQUENCES: 10
- (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: Felfe & Lynch
 - (B) STREET: 805 Third Avenue
 - (C) CITY: New York City
 - (D) STATE: New York
 - (E) COUNTRY: USA
 - (F) ZIP: 10022
- (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Diskette, 3.5 inch, 2.0 MB storage
 - (B) COMPUTER: IBM PS/2
 - (C) OPERATING SYSTEM: PC-DOS
 - (D) SOFTWARE: Wordperfect
- (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER: 08/619,280
 - (B) FILING DATE: 18-MARCH-1996
 - (C) CLASSIFICATION: 435
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: 08/230,491
 - (B) FILING DATE: 20-APRIL-1994
- (viii) ATTORNEY/AGENT INFORMATION:
 - (A) NAME: Hanson, Norman D.
 - (B) REGISTRATION NUMBER: 30,946
 - (C) REFERENCE/DOCKET NUMBER: LUD 5330.1
- (ix) TELECOMMUNICATION INFORMATION:
 - (A) TELEPHONE: (212) 688-9200
 - (B) TELEFAX: (212) 838-3884

(2) INFORMATION FOR SEQ ID NO: 1:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2815 Base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ. ID NO: 1:

AAGAACGCCC	CCAAAATCTG	TTTCTAATTT	TACAGAAATC	TTTTGAAACT	TGGCACGGTA	60
TTCAAAAGTC	CGTGGAAGA	AAAAAACCTT	GTCCTGGCTT	CAGCTTCCAA	CTACAAAGAC	120
AGACTTGGTC	CTTTTCAACG	GTTTTCACAG	ATCCAGTGAC	CCACGCTCTG	AAGACAGAAT	180
TAGCTAACTT	TCAAAAACAT	CTGGAAAAAT	GAAGACTTGG	GTAAAAATCG	TATTTGGAGT	240
TGCCACCTCT	GCTGTGCTTG	CCTTATTGGT	GATGTGCATT	GTCTTACGCC	CTTCAAGAGT	300
TCATAACTCT	GAAGAAAATA	CAATGAGAGC	ACTCACACTG	AAGGATATTT	TAAATGGAAC	360
ATTTTCTTAT	AAAACATTTT	TTCCAAACTG	GATTTTCAGG	CAAGAATATC	TTCATCAATC	420
TGCAGATAAC	AATATAGTAC	TTTATAATAT	TGAAACAGGA	CAATCATATA	CCATTTTGAG	480
TAATAGAACC	ATGAAAAGTG	TGAATGCTTC	AAATTACGGC	TTATCACCTG	ATCGGCAATT	540
TGTATATCTA	GAAAGTGATT	ATTCAAAGCT	TTGGAGATAC	TCTTACACAG	CAACATATTA	600
CATCTATGAC	CTTAGCAATG	GAGAATTTGT	AAGAGGAAAT	GAGCTTCCTC	GTCCAATTCA	660
GTATTTATGC	TGGTCGCCTG	TTGGGAGTAA	ATTAGCATAT	GTCTATCAAA	ACAATATCTA	720
TTTGAAACAA	AGACCAGGAG	ATCCACCTTT	TCAAATAACA	TTTAATGGAA	GAGAAAATAA	780
AATATTTAAT	GGAATCCCAG	ACTGGGTTTA	TGAAGAGGAA	ATGCTTCCTA	CAAAATATGC	840
TCTCTGGTGG	TCTCCTAATG	GAAAATTTTT	GGCATATGCG	GAATTTAATG	ATAAGGATAT	900
ACCAGTTATT	GCCTATTCTT	ATTATGGCGA	TGAACAATAT	CCTAGAACAA	TAAATATTCC	960
ATACCCAAAG	GCTGGAGCTA	AGAATCCCGT	TGTTCCGATA	TTTATTATCG	ATACCACTTA	1020
CCCTGCGTAT	GTAGGTCCCC	AGGAAGTGCC	TGTTCCAGCA	ATGATAGCCT	CAAGTGATTA	1080
TTATTTTCAGT	TGGCTCACGT	GGGTTACTGA	TGAACGAGTA	TGTTTGCAGT	GGCTAAAAAG	1140
AGTCCAGAAT	GTTTCGGTCC	TGTCTATATG	TGACTTCAGG	GAAGACTGGC	AGACATGGGA	1200
TTGTCCAAAG	ACCCAGGAGC	ATATAGAAGA	AAGCAGAACT	GGATGGGCTG	GTGGATTCTT	1260
TGTTTCAAGA	CCAGTTTTC	GCTATGATGC	CATTTTCGTAC	TACAAAATAT	TTAGTGACAA	1320
GGATGGCTAC	AAACATATTC	ACTATATCAA	AGACACTGTG	GAAAATGCTA	TTCAAATTAC	1380
AAGTGGCAAG	TGGGAGGCCA	TAAATATATT	CAGAGTAACA	CAGGATTCAC	TGTTTTATTC	1440
TAGCAATGAA	TTTGAAGAAT	ACCCTGGAAG	AAGAAACATC	TACAGAATTA	GCATTGGAAG	1500
CTATCCTCCA	AGCAAGAAGT	GTGTTACTTG	CCATCTAAGG	AAAGAAAGGT	GCCAATATTA	1560
CACAGCAAGT	TTCAGCGACT	ACGCCAAGTA	CTATGCACTT	GTCTGCTACG	GCCCAGGCAT	1620
CCCCATTTCC	ACCCTTCATG	ATGGACGCAC	TGATCAAGAA	ATTAAAATCC	TGGAAGAAAA	1680
CAAGGAATTG	GAAAATGCTT	TGAAAAATAT	CCAGCTGCCT	AAAGAGGAAA	TTAAGAAACT	1740
TGAAGTAGAT	GAAATTACTT	TATGGTACAA	GATGATTCTT	CCTCCTCAAT	TTGACAGATC	1800
AAAGAAGTAT	CCCTTGCTAA	TTCAAGTGTA	TGGTGGTCCC	TGCAGTCAGA	GTGTAAGGTC	1860
TGTATTTGCT	GTTAATTGGA	TATCTTATCT	TGCAAGTAAG	GAAGGGATGG	TCATTGCCTT	1920
GGTGGATGGT	CGAGGAACAG	CTTTCCAAGG	TGACAAACTC	CTCTATGCAG	TGTATCGAAA	1980
GCTGGGTGTT	TATGAAGTTG	AAGACCAGAT	TACAGCTGTC	AGAAAATTCA	TAGAAATGGG	2040
TTTCATTGAT	GAAAAAAGAA	TAGCCATATG	GGGCTGGTCC	TATGGAGGAT	ACGTTTCATC	2100
ACTGGCCCTT	GCATCTGGAA	CTGGTCTTTT	CAAATGTGGT	ATAGCAGTGG	CTCCAGTCTC	2160
CAGCTGGGAA	TATTACGCGT	CTGTCTACAC	AGAGAGATTC	ATGGGTCTCC	CAACAAAGGA	2220
TGATAATCTT	GAGCACTATA	AGAATTCAAC	TGTGATGGCA	AGAGCAGAAT	ATTTTCAGAAA	2280
TGTAGACTAT	CTTCTCATCC	ACGGAACAGC	AGATGATAAT	GTGCACTTTC	AAAACCTCAGC	2340
ACAGATTGCT	AAAGCTCTGG	TTAATGCACA	AGTGGATTTC	CAGGCAATGT	GGTACTCTGA	2400
CCAGAACCAC	GGCTTATCCG	GCCTGTCCAC	GAACCACTTA	TACACCCACA	TGACCCACTT	2460
CCTAAAGCAG	TGTTTCTCTT	TGTCAGACTA	AAAACGATGC	AGATGCAAGC	CTGTATCAGA	2520
ATCTGAAAAC	CTTATATAAA	CCCCTCAGAC	AGTTTGCTTA	TTTTATTTTT	TATGTTGTAA	2580
AATGCTAGTA	TAAACAAACA	AATTAATGTT	GTTCTAAAGG	CTGTTAAAAA	AAAGATGAGG	2640
ACTCAGAAGT	TCAAGCTAAA	TATTGTTTAC	ATTTTCTGGT	ACTCTGTGAA	AGAAGAGAAA	2700

AGGGAGTCAT GCATTTTGCT TTGGACACAG TGTTTTATCA CCTGTTCATT TGAAGAAAAA 2760
 TAATAAAGTC AGAAGTTCAA AAAAAAAAAA AAAAAAAAAA AAAGCGGCCG CTCGA 2815

(2) INFORMATION FOR SEQ ID NO: 2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 760 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

Met	Lys	Thr	Trp	Val	Lys	Ile	Val	Phe	Gly	Val	Ala	Thr	Ser	Ala	Val	5	10	15
Leu	Ala	Leu	Leu	Val	Met	Cys	Ile	Val	Leu	Arg	Pro	Ser	Arg	Val	His	20	25	30
Asn	Ser	Glu	Glu	Asn	Thr	Met	Arg	Ala	Leu	Thr	Leu	Lys	Asp	Ile	Leu	35	40	45
Asn	Gly	Thr	Phe	Ser	Tyr	Lys	Thr	Phe	Phe	Pro	Asn	Trp	Ile	Ser	Gly	50	55	60
Gln	Glu	Tyr	Leu	His	Gln	Ser	Ala	Asp	Asn	Asn	Ile	Val	Leu	Tyr	Asn	65	70	75
Ile	Glu	Thr	Gly	Gln	Ser	Tyr	Thr	Ile	Leu	Ser	Asn	Arg	Thr	Met	Lys	85	90	95
Ser	Val	Asn	Ala	Ser	Asn	Tyr	Gly	Leu	Ser	Pro	Asp	Arg	Gln	Phe	Val	100	105	110
Tyr	Leu	Glu	Ser	Asp	Tyr	Ser	Lys	Leu	Trp	Arg	Tyr	Ser	Tyr	Thr	Ala	115	120	125
Thr	Tyr	Tyr	Ile	Tyr	Asp	Leu	Ser	Asn	Gly	Glu	Phe	Val	Arg	Gly	Asn	130	135	140
Glu	Leu	Pro	Arg	Pro	Ile	Gln	Tyr	Leu	Cys	Trp	Ser	Pro	Val	Gly	Ser	145	150	155
Lys	Leu	Ala	Tyr	Val	Tyr	Gln	Asn	Asn	Ile	Tyr	Leu	Lys	Gln	Arg	Pro	165	170	175
Gly	Asp	Pro	Pro	Phe	Gln	Ile	Thr	Phe	Asn	Gly	Arg	Glu	Asn	Lys	Ile	180	185	190
Phe	Asn	Gly	Ile	Pro	Asp	Trp	Val	Tyr	Glu	Glu	Glu	Met	Leu	Pro	Thr	195	200	205
Lys	Tyr	Ala	Leu	Trp	Trp	Ser	Pro	Asn	Gly	Lys	Phe	Leu	Ala	Tyr	Ala	210	215	220

Glu 225	Phe	Asn	Asp	Lys	Asp 230	Ile	Pro	Val	Ile	Ala 235	Tyr	Ser	Tyr	Tyr	Gly 240
Asp	Glu	Gln	Tyr	Pro 245	Arg	Thr	Ile	Asn	Ile 250	Pro	Tyr	Pro	Lys	Ala	Gly 255
Ala	Lys	Asn	Pro 260	Val	Val	Arg	Ile	Phe 265	Ile	Ile	Asp	Thr	Thr	Tyr	Pro
Ala	Tyr	Val 275	Gly	Pro	Gln	Glu	Val 280	Pro	Val	Pro	Ala	Met 285	Ile	Ala	Ser
Ser 290	Asp	Tyr	Tyr	Phe	Ser	Trp 295	Leu	Thr	Trp	Val	Thr	Asp	Glu	Arg	Val
Cys 305	Leu	Gln	Trp	Leu	Lys 310	Arg	Val	Gln	Asn	Val 315	Ser	Val	Leu	Ser	Ile 320
Cys	Asp	Phe	Arg	Glu 325	Asp	Trp	Gln	Thr	Trp 330	Asp	Cys	Pro	Lys	Thr	Gln 335
Glu	His	Ile	Glu 340	Glu	Ser	Arg	Thr	Gly 345	Trp	Ala	Gly	Gly	Phe	Phe	Val
Ser	Arg	Pro 355	Val	Phe	Ser	Tyr	Asp 360	Ala	Ile	Ser	Tyr	Tyr 365	Lys	Ile	Phe
Ser 370	Asp	Lys	Asp	Gly	Tyr	Lys 375	His	Ile	His	Tyr	Ile 380	Lys	Asp	Thr	Val
Glu 385	Asn	Ala	Ile	Gln 390	Ile	Thr	Ser	Gly	Lys	Trp 395	Glu	Ala	Ile	Asn	Ile 400
Phe	Arg	Val	Thr 405	Gln	Asp	Ser	Leu	Phe 410	Tyr	Ser	Ser	Asn	Glu	Phe	Glu 415
Glu	Tyr	Pro 420	Gly	Arg	Arg	Asn	Ile	Tyr 425	Arg	Ile	Ser	Ile	Gly 430	Ser	Tyr
Pro	Pro	Ser 435	Lys	Lys	Cys	Val	Thr 440	Cys	His	Leu	Arg	Lys	Glu	Arg	Cys 445
Gln	Tyr 450	Tyr	Thr	Ala	Ser	Phe 455	Ser	Asp	Tyr	Ala	Lys	Tyr	Tyr	Ala	Leu
Val 465	Cys	Tyr	Gly	Pro	Gly 470	Ile	Pro	Ile	Ser	Thr 475	Leu	His	Asp	Gly	Arg 480
Thr	Asp	Gln	Glu 485	Ile	Lys	Ile	Leu	Glu	Glu 490	Asn	Lys	Glu	Leu	Glu	Asn 495
Ala	Leu	Lys	Asn 500	Ile	Gln	Leu	Pro	Lys 505	Glu	Glu	Ile	Lys	Lys	Leu	Glu 510

Val Asp Glu Ile Thr Leu Trp Tyr Lys Met Ile Leu Pro Pro Gln Phe
515 520 525

Asp Arg Ser Lys Lys Tyr Pro Leu Leu Ile Gln Val Tyr Gly Gly Pro
530 535 540

Cys Ser Gln Ser Val Arg Ser Val Phe Ala Val Asn Trp Ile Ser Tyr
545 550 555 560

Leu Ala Ser Lys Glu Gly Met Val Ile Ala Leu Val Asp Gly Arg Gly -
565 570 575

Thr Ala Phe Gln Gly Asp Lys Leu Leu Tyr Ala Val Tyr Arg Lys Leu
580 585 590

Gly Val Tyr Glu Val Glu Asp Gln Ile Thr Ala Val Arg Lys Phe Ile
595 600 605

Glu Met Gly Phe Ile Asp Glu Lys Arg Ile Ala Ile Trp Gly Trp Ser
610 615 620

Tyr Gly Gly Tyr Val Ser Ser Leu Ala Leu Ala Ser Gly Thr Gly Leu
625 630 635 640

Phe Lys Cys Gly Ile Ala Val Ala Pro Val Ser Ser Trp Glu Tyr Tyr
645 650 655

Ala Ser Val Tyr Thr Glu Arg Phe Met Gly Leu Pro Thr Lys Asp Asp
660 665 670

Asn Leu Glu His Tyr Lys Asn Ser Thr Val Met Ala Arg Ala Glu Tyr
675 680 685

Phe Arg Asn Val Asp Tyr Leu Leu Ile His Gly Thr Ala Asp Asp Asn
690 695 700

Val His Phe Gln Asn Ser Ala Gln Ile Ala Lys Ala Leu Val Asn Ala
705 710 715 720

Gln Val Asp Phe Gln Ala Met Trp Tyr Ser Asp Gln Asn His Gly Leu
725 730 735

Ser Gly Leu Ser Thr Asn His Leu Tyr Thr His Met Thr His Phe Leu
740 745 750

Lys Gln Cys Phe Ser Leu Ser Asp
755 760

(2) INFORMATION FOR SEQ ID NO: 3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 766 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

Met Lys Thr Pro Trp Lys Val Leu Leu Gly Leu Leu Gly Ala Ala Ala .
5 10 15

Leu Val Thr Ile Ile Thr Val Pro Val Val Leu Leu Asn Lys Gly Thr
20 25 30

Asp Asp Ala Thr Ala Asp Ser Arg Lys Thr Tyr Thr Leu Thr Asp Tyr
35 40 45

Leu Lys Asn Thr Tyr Arg Leu Lys Leu Tyr Ser Leu Arg Trp Ile Ser
50 55 60

Asp His Glu Tyr Leu Tyr Lys Gln Glu Asn Asn Ile Leu Val Phe Asn
65 70 75 80

Ala Glu Tyr Gly Asn Ser Ser Val Phe Leu Glu Asn Ser Thr Phe Asp
85 90 95

Glu Phe Gly His Ser Ile Asn Asp Tyr Ser Ile Ser Pro Asp Gly Gln
100 105 110

Phe Ile Leu Leu Glu Tyr Asn Tyr Val Lys Gln Trp Arg His Ser Tyr
115 120 125

Thr Ala Ser Tyr Asp Ile Tyr Asp Leu Asn Lys Arg Gln Leu Ile Thr
130 135 140

Glu Glu Arg Ile Pro Asn Asn Thr Gln Trp Val Thr Trp Ser Pro Val
145 150 155 165

Gly His Lys Leu Ala Tyr Val Trp Asn Asn Asp Ile Tyr Val Lys Ile
170 175 180

Glu Pro Asn Leu Pro Ser Tyr Arg Ile Thr Trp Thr Gly Lys Glu Asp
185 190 195

Ile Ile Tyr Asn Gly Ile Thr Asp Trp Val Tyr Glu Glu Glu Val Phe
200 205 210

Ser Ala Tyr Ser Ala Leu Trp Trp Ser Pro Asn Gly Thr Phe Leu Ala
215 220 225

Tyr Ala Gln Phe Asn Asp Thr Glu Val Pro Leu Ile Glu Tyr Ser Phe
230 235 240 245

Tyr	Ser	Asp	Glu	Ser	Leu	Gln	Tyr	Pro	Lys	Thr	Val	Arg	Val	Pro	Tyr
				250					255					260	
Pro	Lys	Ala	Gly	Ala	Val	Asn	Pro	Thr	Val	Lys	Phe	Phe	Val	Val	Asn
			265					270					275		
Thr	Asp	Ser	Leu	Ser	Ser	Val	Thr	Asn	Ala	Thr	Ser	Ile	Gln	Ile	Thr
		280					285					290			
Ala	Pro	Ala	Ser	Met	Leu	Ile	Gly	Asp	His	Tyr	Leu	Cys	Asp	Val	Thr
	295					300					305				
Trp	Ala	Thr	Gln	Glu	Arg	Ile	Ser	Leu	Gln	Trp	Leu	Arg	Arg	Ile	Gln
310					315					320				325	
Asn	Tyr	Ser	Val	Met	Asp	Ile	Cys	Asp	Tyr	Asp	Glu	Ser	Ser	Gly	Arg
				330					335					340	
Trp	Asn	Cys	Leu	Val	Ala	Arg	Gln	His	Ile	Glu	Met	Ser	Thr	Thr	Gly
			345					350					355		
Trp	Val	Gly	Arg	Phe	Arg	Pro	Ser	Glu	Pro	His	Phe	Thr	Leu	Asp	Gly
		360					365					370			
Asn	Ser	Phe	Tyr	Lys	Ile	Ile	Ser	Asn	Glu	Glu	Gly	Tyr	Arg	His	Ile
		375				380					385				
Cys	Tyr	Phe	Gln	Ile	Asp	Lys	Lys	Asp	Cys	Thr	Phe	Ile	Thr	Lys	Gly
390					395					400				405	
Thr	Trp	Glu	Val	Ile	Gly	Ile	Glu	Ala	Leu	Thr	Ser	Asp	Tyr	Leu	Tyr
				410					415					420	
Tyr	Ile	Ser	Asn	Glu	Tyr	Lys	Gly	Met	Pro	Gly	Gly	Arg	Asn	Leu	Tyr
			425					430					435		
Lys	Ile	Gln	Leu	Ser	Asp	Tyr	Thr	Lys	Val	Thr	Cys	Leu	Ser	Cys	Glu
		440					445					450			
Leu	Asn	Pro	Glu	Arg	Cys	Gln	Tyr	Tyr	Ser	Val	Ser	Phe	Ser	Lys	Glu
	455					460					460				
Ala	Lys	Tyr	Tyr	Gln	Leu	Arg	Cys	Ser	Gly	Pro	Gly	Leu	Pro	Leu	Tyr
465					470					475				480	
Thr	Leu	His	Ser	Ser	Val	Asn	Asp	Lys	Gly	Leu	Arg	Val	Leu	Glu	Asp
			485						490					495	
Asn	Ser	Ala	Leu	Asp	Lys	Met	Leu	Gln	Asn	Val	Gln	Met	Pro	Ser	Lys
			500					505					510		
Lys	Leu	Asp	Phe	Ile	Ile	Leu	Asn	Glu	Thr	Lys	Phe	Trp	Tyr	Gln	Met
		515					520					525			

Ile Leu Pro Pro His Phe Asp Lys Ser Lys Lys Tyr Pro Leu Leu Leu
530 535 540

Asp Val Tyr Ala Gly Pro Cys Ser Gln Lys Ala Asp Thr Val Phe Arg
545 550 555 560

Leu Asn Trp Ala Thr Tyr Leu Ala Ser Thr Glu Asn Ile Ile Val Ala
565 570 575

Ser Phe Asp Gly Arg Gly Ser Gly Tyr Gln Gly Asp Lys Ile Met His
580 585 590

Ala Ile Asn Arg Arg Leu Gly Thr Phe Glu Val Glu Asp Gln Ile Glu
595 600 605

Ala Ala Arg Gln Phe Ser Lys Met Gly Phe Val Asp Asn Lys Arg Ile
610 615 620

Ala Ile Trp Gly Trp Ser Tyr Gly Gly Tyr Val Thr Ser Met Val Leu
625 630 635 640

Gly Ser Gly Ser Gly Val Phe Lys Cys Gly Ile Ala Val Ala Pro Val
645 650 655

Ser Arg Trp Glu Tyr Tyr Asp Ser Val Tyr Thr Glu Arg Tyr Met Gly
660 665 670

Leu Pro Thr Pro Glu Asp Asn Leu Asp His Tyr Arg Asn Ser Thr Val
675 680 685

Met Ser Arg Ala Glu Asn Phe Lys Gln Val Glu Tyr Leu Leu Ile His
690 695 700

Gly Thr Ala Asp Asp Asn Val His Phe Gln Gln Ser Ala Gln Ile Ser
705 710 715 720

Lys Ala Leu Val Asp Val Gly Val Asp Phe Gln Ala Met Trp Tyr Thr
725 730 735

Asp Glu Asp His Gly Ile Ala Ser Ser Thr Ala His Gln His Ile Tyr
740 745 750

Thr His Met Ser His Phe Ile Lys Gln Cys Phe Ser Leu Pro
755 760 765

- (2) INFORMATION FOR SEQ ID NO: 4:
(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 7 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
(ix) FEATURE:
 (D) OTHER INFORMATION: The first Xaa is either Trp or Phe.
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

Xaa Gly Trp Ser Tyr Gly Gly
5

- (2) INFORMATION FOR SEQ ID NO: 5:
(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 7 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

Phe Gly Lys Asp Tyr Gly Gly
5

- (2) INFORMATION FOR SEQ ID NO: 6:
(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 7 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
(ix) FEATURE:
 (D) OTHER INFORMATION: Xaa is either Ala or Gly
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:

Gly Thr Xaa Asp Asp Asn Val
5

- (2) INFORMATION FOR SEQ ID NO: 7:
(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 7 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:

Ala Gln Asn His Gly Leu Ser
5

- (2) INFORMATION FOR SEQ ID NO: 8:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 7 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
(ix) FEATURE:
 (D) OTHER INFORMATION:
 The first Xaa is Glu or Ser. When the first Xaa is Glu,
 the second Xaa is Gly and the third is Ala. When the
 first Xaa is Ser, the second Xaa is Ser, and the third
 Xaa is Arg.
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:

Asp Xaa Asp His Xaa Ile Xaa
5

- (2) INFORMATION FOR SEQ ID NO: 9:
(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 7 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
(ix) FEATURE:
 (D) OTHER INFORMATION:
 Xaa is Pro or Ala.
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:

Xaa Thr Ala Asp Glu Lys Ile
5

- (2) INFORMATION FOR SEQ ID NO: 10:
(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 7 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
(ix) FEATURE:
 (D) OTHER INFORMATION:
 Xaa is Thr, His or Ser.
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10:

Asp Glu Ser His Tyr Phe Xaa
5